

Laser capture microdissection (LCM) and expressed sequence tag analysis of the syncytium formed by the soybean cyst nematode *Heterodera glycines* in *Glycine max* (soybean).

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ABSTRACT

Laser capture microdissection (LCM) was used to isolate nematode feeding sites (syncytia) from susceptible soybean (*Glycine max* L. Merr. Kent) roots inoculated with the soybean cyst nematode (SCN), *Heterodera glycines* Ichinohe. RNA was extracted from the syncytia and a cDNA library was constructed for expressed sequence tag (EST), analyses. The ~700 ESTs fall into 174 contigs. Approximately ten percent of the contigs are homologous to wound/pathogen-induced or syncytium enhanced genes. Approximately 33% of the contigs have homology to genes involved in a variety of cellular processes in plants. Approximately 15% of the contigs are either predicted proteins or are ESTs found only in soybeans. Another 42% of the contigs have no significant identity with any sequence. These data demonstrate that LCM can be used to microdissect the developing syncytium, specifically providing tissue suitable for mRNA preparation. The mRNA extracted from the developing syncytium has been used to identify genes that exhibit expression within and around the syncytium. More broadly, LCM can be used to investigate plant-pathogen interactions where spatial domains are difficult to separate.